SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Weeks, Donald P.
                Wang, Xiao-Zhuo
                Herman, Patricia L.

    (ii) TITLE OF INVENTION: "METHODS AND MATERIALS FOR MAKING AND
          USING TRANSGENIC DICAMBA-DEGRADING ORGANISMS"

    (iii) NUMBER OF SEQUENCES: 6

    (iv) CORRESPONDENCE ADDRESS:
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        (D) STATE: Colorado
        (E) COUNTRY: USA
        (F) ZIP: 80203

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER:
        (B) FILING DATE:
        (C) CLASSIFICATION:

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 60/042,666
        (B) FILING DATE: 04-APR-1997

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 60/042,941
        (B) FILING DATE: 04-APR-1997

    (viii) ATTORNEY/AGENT INFORMATION:
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        (B) REGISTRATION NUMBER: 31,071
        (C) REFERENCE/DOCKET NUMBER: 3553-18

    (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 29 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (ix) FEATURE:
        (A) NAME/KEY: Region
        (B) LOCATION: 28
        (D) OTHER INFORMATION: /note= "Best guess for Xaa = Asp or
Thr"

    (ix) FEATURE:
        (A) NAME/KEY: Region
        (B) LOCATION: 29
        (D) OTHER INFORMATION: /note= "Best guess for Xaa = Pro"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu Leu
1   5   10   15

Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Xaa Xaa
          20   25

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (ix) FEATURE:
        (A) NAME/KEY: Region
        (B) LOCATION: 8
        (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

    (ix) FEATURE:
        (A) NAME/KEY: Region
        (B) LOCATION: 11
        (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

    (ix) FEATURE:
        (A) NAME/KEY: Region
        (B) LOCATION: 16
        (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

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(ix) FEATURE:
     (A) NAME/KEY: Region
     (B) LOCATION: 20
     (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Thr Tyr Val Val Thr Asp Ala Xaa Ile Lys Xaa Lys Tyr Met Asp Xaa
1               5                   10                  15


Val Glu Val Xaa
          20




(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1020 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (ix) FEATURE:
         (A) NAME/KEY: CDS
         (B) LOCATION: 1..1020


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG ACC TTC GTC CGC AAT GCC TGG TAT GTG GCG GCG CTG CCC GAG GAA        48
Met Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu
 1               5                   10                  15

CTG TCC GAA AAG CCG CTC GGC CGG ACG ATT CTC GAC ACA CCG CTC GCG        96
Leu Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Thr Pro Leu Ala
            20                  25                  30

CTC TAC CGC CAG CCC GAC GGT GTG GTC GCG GCG CTG CTC GAC ATC TGT       144
Leu Tyr Arg Gln Pro Asp Gly Val Val Ala Ala Leu Leu Asp Ile Cys
        35                  40                  45

CCG CAC CGC TTC GCG CCG CTG AGC GAC GGC ATC CTC GTC AAC GGC CAT       192
Pro His Arg Phe Ala Pro Leu Ser Asp Gly Ile Leu Val Asn Gly His
    50                  55                  60

CTC CAA TGC CCC TAT CAC GGG CTG GAA TTC GAT GGC GGC GGG CAG TGC       240
Leu Gln Cys Pro Tyr His Gly Leu Glu Phe Asp Gly Gly Gly Gln Cys
65                  70                  75                  80

GTC CAT AAC CCG CAC GGC AAT GGC GCC CGC CCG GCT TCG CTC AAC GTC       288
Val His Asn Pro His Gly Asn Gly Ala Arg Pro Ala Ser Leu Asn Val
        85                  90                  95
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58

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CGC TCC TTC CCG GTG GTG GAG CGC GAC GCG CTG ATC TGG ATC TGG CCC         336
Arg Ser Phe Pro Val Val Glu Arg Asp Ala Leu Ile Trp Ile Trp Pro
        100                 105                 110

GGC GAT CCG GCG CTG GCC GAT CCT GGG GCG ATC CCC GAC TTC GGC TGC         384
Gly Asp Pro Ala Leu Ala Asp Pro Gly Ala Ile Pro Asp Phe Gly Cys
        115                 120                 125

CGC GTC GAT CCC GCC TAT CGG ACC GTC GGC GGC TAT GGG CAT GTC GAC         432
Arg Val Asp Pro Ala Tyr Arg Thr Val Gly Gly Tyr Gly His Val Asp
        130                 135                 140

TGC AAC TAC AAG CTG CTG GTC GAC AAC CTG ATG GAC CTC GGC CAC GCC         480
Cys Asn Tyr Lys Leu Leu Val Asp Asn Leu Met Asp Leu Gly His Ala
145                 150                 155                 160

CAA TAT GTC CAT CGC GCC AAC GCC CAG ACC GAC GCC TTC GAC CGG CTG         528
Gln Tyr Val His Arg Ala Asn Ala Gln Thr Asp Ala Phe Asp Arg Leu
                165                 170                 175

GAG CGC GAG GTG ATC GTC GGC GAC GGT GAG ATA CAG GCG CTG ATG AAG         576
Glu Arg Glu Val Ile Val Gly Asp Gly Glu Ile Gln Ala Leu Met Lys
        180                 185                 190

ATT CCC GGC GGC ACG CCG AGC GTG CTG ATG GCC AAG TTC CTG CGC GGC         624
Ile Pro Gly Gly Thr Pro Ser Val Leu Met Ala Lys Phe Leu Arg Gly
        195                 200                 205

GCC AAT ACC CCC GTC GAC GCT TGG AAC GAC ATC CGC TGG AAC AAG GTG         672
Ala Asn Thr Pro Val Asp Ala Trp Asn Asp Ile Arg Trp Asn Lys Val
        210                 215                 220

AGC GCG ATG CTC AAC TTC ATC GCG GTG GCG CCG GAA GGC ACC CCG AAG         720
Ser Ala Met Leu Asn Phe Ile Ala Val Ala Pro Glu Gly Thr Pro Lys
225                 230                 235                 240

GAG CAG AGC ATC CAC TCG CGC GGT ACC CAT ATC CTG ACC CCC GAG ACG         768
Glu Gln Ser Ile His Ser Arg Gly Thr His Ile Leu Thr Pro Glu Thr
                245                 250                 255

GAG GCG AGC TGC CAT TAT TTC TTC GGC TCC TCG CGC AAT TTC GGC ATC         816
Glu Ala Ser Cys His Tyr Phe Phe Gly Ser Ser Arg Asn Phe Gly Ile
        260                 265                 270

GAC GAT CCG GAG ATG GAC GGC GTG CTG CGC AGC TGG CAG GCT CAG GCG         864
Asp Asp Pro Glu Met Asp Gly Val Leu Arg Ser Trp Gln Ala Gln Ala
        275                 280                 285

CTG GTC AAG GAG GAC AAG GTC GTC GTC GAG GCG ATC GAG CGC CGC CGC         912
Leu Val Lys Glu Asp Lys Val Val Val Glu Ala Ile Glu Arg Arg Arg
        290                 295                 300

GCC TAT GTC GAG GCG AAT GGC ATC CGC CCG GCG ATG CTG TCG TGC GAC         960
Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
305                 310                 315                 320
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59

```
GAA GCC GCA GTC CGT GTC AGC CGC GAG ATC GAG AAG CTT GAG CAG CTC    1008
Glu Ala Ala Val Arg Val Ser Arg Glu Ile Glu Lys Leu Glu Gln Leu
            325             330             335

GAA GCC GCC TGA                                                    1020
Glu Ala Ala  *
        340
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 340 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu
 1           5               10              15

Leu Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Thr Pro Leu Ala
            20              25              30

Leu Tyr Arg Gln Pro Asp Gly Val Val Ala Ala Leu Leu Asp Ile Cys
        35              40              45

Pro His Arg Phe Ala Pro Leu Ser Asp Gly Ile Leu Val Asn Gly His
    50              55              60

Leu Gln Cys Pro Tyr His Gly Leu Glu Phe Asp Gly Gly Gly Gln Cys
65              70              75              80

Val His Asn Pro His Gly Asn Gly Ala Arg Pro Ala Ser Leu Asn Val
            85              90              95

Arg Ser Phe Pro Val Val Glu Arg Asp Ala Leu Ile Trp Ile Trp Pro
            100             105             110

Gly Asp Pro Ala Leu Ala Asp Pro Gly Ala Ile Pro Asp Phe Gly Cys
        115             120             125

Arg Val Asp Pro Ala Tyr Arg Thr Val Gly Gly Tyr Gly His Val Asp
    130             135             140

Cys Asn Tyr Lys Leu Leu Val Asp Asn Leu Met Asp Leu Gly His Ala
145             150             155             160

Gln Tyr Val His Arg Ala Asn Ala Gln Thr Asp Ala Phe Asp Arg Leu
            165             170             175

Glu Arg Glu Val Ile Val Gly Asp Gly Glu Ile Gln Ala Leu Met Lys
            180             185             190
```

```
Ile Pro Gly Gly Thr Pro Ser Val Leu Met Ala Lys Phe Leu Arg Gly
        195             200             205

Ala Asn Thr Pro Val Asp Ala Trp Asn Asp Ile Arg Trp Asn Lys Val
        210             215             220

Ser Ala Met Leu Asn Phe Ile Ala Val Ala Pro Glu Gly Thr Pro Lys
225             230             235             240

Glu Gln Ser Ile His Ser Arg Gly Thr His Ile Leu Thr Pro Glu Thr
            245             250             255

Glu Ala Ser Cys His Tyr Phe Phe Gly Ser Ser Arg Asn Phe Gly Ile
            260             265             270

Asp Asp Pro Glu Met Asp Gly Val Leu Arg Ser Trp Gln Ala Gln Ala
        275             280             285

Leu Val Lys Glu Asp Lys Val Val Val Glu Ala Ile Glu Arg Arg Arg
    290             295             300

Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
305             310             315             320

Glu Ala Ala Val Arg Val Ser Arg Glu Ile Glu Lys Leu Glu Gln Leu
            325             330             335

Glu Ala Ala  *
        340
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 339 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..339

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
ATG ACC TAT GTC GTC ACC GAC GCC TGC ATC AAG TGC AAG TAC ATG GAC    48
Met Thr Tyr Val Val Thr Asp Ala Cys Ile Lys Cys Lys Tyr Met Asp
 1               5               10              15

TGC GTG GAA GTC TGC CCT GTG GAC TGC TTC TAC GAA GGC GAG AAC ATG    96
Cys Val Glu Val Cys Pro Val Asp Cys Phe Tyr Glu Gly Glu Asn Met
            20              25              30
```

```
CTC GTC ATC AAT CCC AGT GAA TGC ATC GAC TGC GGC GTC TGC GAA CCG    144
Leu Val Ile Asn Pro Ser Glu Cys Ile Asp Cys Gly Val Cys Glu Pro
        35                  40                  45

GAA TGC CCA GCC GAA GCC ATC CTT CCC GAC ACC GAA AGC GGT CTC GAG    192
Glu Cys Pro Ala Glu Ala Ile Leu Pro Asp Thr Glu Ser Gly Leu Glu
    50                  55                  60

CAG TGG ATG GAA CTG AAC ACG AAG TAC TCG GCC GAG TGG CCG AAT CTC    240
Gln Trp Met Glu Leu Asn Thr Lys Tyr Ser Ala Glu Trp Pro Asn Leu
65                  70                  75                  80

ACG TCC AAG AAA GAT TCG CCG GAA GAT GCC GAC GAG TAC AAG GGC GTG    288
Thr Ser Lys Lys Asp Ser Pro Glu Asp Ala Asp Glu Tyr Lys Gly Val
                85                  90                  95

GAA GGC AAG TTC GAG AAG TTC TTC TCG CCC GAG CCC GGC GAG GGC GAC    336
Glu Gly Lys Phe Glu Lys Phe Phe Ser Pro Glu Pro Gly Glu Gly Asp
            100                 105                 110

TGA                                                                339
*
```

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Thr Tyr Val Val Thr Asp Ala Cys Ile Lys Cys Lys Tyr Met Asp
 1               5                  10                  15

Cys Val Glu Val Cys Pro Val Asp Cys Phe Tyr Glu Gly Glu Asn Met
            20                  25                  30

Leu Val Ile Asn Pro Ser Glu Cys Ile Asp Cys Gly Val Cys Glu Pro
        35                  40                  45

Glu Cys Pro Ala Glu Ala Ile Leu Pro Asp Thr Glu Ser Gly Leu Glu
    50                  55                  60

Gln Trp Met Glu Leu Asn Thr Lys Tyr Ser Ala Glu Trp Pro Asn Leu
65                  70                  75                  80

Thr Ser Lys Lys Asp Ser Pro Glu Asp Ala Asp Glu Tyr Lys Gly Val
                85                  90                  95

Glu Gly Lys Phe Glu Lys Phe Phe Ser Pro Glu Pro Gly Glu Gly Asp
            100                 105                 110

*
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